

Conseiller.ST25
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel
Debussche, Laurent
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 5'-1(p53)

<400> 1
agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 3' -393 (p53)

Conseiller.ST25

<400> 2
agatctcatc agtctgagtc agggccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide H175 3'

<400> 3
ggggcagtgc ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide W248 3'

<400> 4
gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide H273 3'

<400> 5
acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

Conseiller.ST25

<213> Artificial Sequence

<220>
<223> oligonucleotide G281 3'

<400> 6
gcgcggcct ccccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 5'-73

<400> 7
agatctgtgt ggccctgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>
<223> Murine MBP1 C-term fragment

<220>
<221> CDS
<222> (1)..(885)

<400> 8
tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac 48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg 96
Ile Asp Glu Cys Arg Tyr Arg Cys Gln His Arg Cys Val Asn Leu
20 25 30

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct 144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca 192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt 240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
Page 3

Conseiller.ST25

65	70	75	80	
aac	cag	ggc	tat	288
Asn	Gln	Gly	Tyr	
85	Glu	Leu	His	
	Arg	Asp	Gly	
		Phe	Ser	
		Cys	Ser	
			Asp	
			Ile	
		90	95	
gat	gag	tgc	gac	336
Asp	Glu	Cys	Gly	
100	Tyr	Ser	Tyr	
			Leu	
			Cys	
		105	110	
gag	cca	ggc	cga	384
Glu	Pro	Gly	Arg	
115	Phe	Ser	Cys	
			His	
		120	125	
gct	aca	agg	ctc	432
Ala	Thr	Arg	Tyr	
130	Leu	Cys	Gln	
			Asp	
			Ile	
		135	140	
caa	tgt	tct	gag	480
Gln	Cys	Ser	Glu	
145	Ala	Gln	Thr	
			Cys	
		150	155	
			Val	
			Asn	
			Phe	
			His	
			Gly	
			Tyr	
			Arg	
			160	
tgt	gtg	gac	acc	528
Cys	Val	Asp	Thr	
165	Asn	Arg	Cys	
			Val	
		170	175	
aac	cgc	tgc	ctc	576
Asn	Arg	Cys	Leu	
180	Cys	Pro	Ala	
			Ser	
		185	190	
tca	tcc	att	gtg	624
Ser	Ser	Ile	Val	
195	His	Arg	Tyr	
		Met	Ser	
		200	205	
cct	gct	gac	gtg	672
Pro	Ala	Asp	Val	
210	Phe	Gln	Ile	
			Gln	
		215	220	
			Ala	
tac	aat	gcc	ttt	720
Tyr	Asn	Ala	Phe	
225	Gln	Ile	Arg	
			Ser	
		230	235	
			Gly	
			Asn	
			Thr	
			Gly	
			Asp	
			Phe	
			Tyr	
			240	
att	agg	caa	atc	768
Ile	Arg	Gln	Ile	
245	Asn	Val	Ser	
			Ala	
		250	255	
atg	acg	gga	ccc	816
Val	Thr	Gly	Pro	
260	Arg	Glu	Tyr	
		265	270	
aat	tcc	ctt	atg	864
Asn	Ser	Leu	Met	
275	Met	Ser	Tyr	
			Arg	
		280	285	
ttt	gtg	gga	gcc	915
Phe	Val	Gly	Ala	
290	Tyr	Thr	Phe	
		295		
ggccctcc	cctccatag	cttaagcgc	cccgggggcc	975
aaaggaacta	tgtatgtaa	gacaataaag	ggagaaagaa	1021
aaaggaacta	tgtatgtaa	gacaataaag	ggagaaagaa	

Conseiller.ST25

<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Conseiller ST25
Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220> <223> Oligonucleotide c-myc 5'

<400> 10 gatccatgga gcagaagctg atctccgagg aggacctga 39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220> <223> Oligonucleotide c-myc 3'

<400> 11 gatctcagggt cctcctcgga gatcagcttc tgctccatg 39

<210> 12

Conseiller.ST25

<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' MCS oligonucleotide

<400> 12
gatctcggtc gacctgcattt caattccggg gtgcggccgc gagct

45

<210> 13
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' MCS oligonucleotide

<400> 13
cgcggccgc cccggaaattt gcatgcaggcgaccga

37

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide 3' mMBP1

<400> 14
cggtaactggc agaggtaact gg

22

<210> 15
<211> 1513
<212> DNA
<213> Artificial Sequence
<220>
<223> MBP1 murine (complete sequence)
<220>
<221> CDS
<222> (49)..(1377)

Conseiller ST25

<400> 15 gctgtggcag aaacccctga cttctgccc ccacccccc gcctcagg atg ctc cct
 Met Leu Pro 1
 ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg 105
 Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu
 5 10 15
 ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccc gac agc
 153
 Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser
 20 25 30 35
 tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac
 201
 Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His
 40 45 50
 tgc cgg gat gtc aac gag tgc ctg acc atc ccc gag gct tgc aag ggt
 249
 Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly
 55 60 65
 gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctc cct cgc
 297
 Glu Met Lys Cys Ile Asn His Tyr Gly Tyr Leu Cys Leu Pro Arg
 70 75 80
 tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccc cca
 345
 Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro
 85 90 95
 gcg gcc cat gct caa caa cca aac cct tgc ccc cag ggc tac gag cct
 393
 Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro
 100 105 110 115
 gat gaa cag gag agc tgt gtc gat gtc gac gag tgt acc cag gct ttg
 441
 Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu
 120 125 130
 cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac
 489
 His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr
 135 140 145
 cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtc
 537
 Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val
 150 155 160
 gag ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtc aac
 585
 Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn
 165 170 175
 ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga
 633
 Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly
 180 185 190 195
 cct aac aac cgc tct tgt gtc gat gtc aat gag tgt gac atg gga gcc
 681
 Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala
 200 205 210
 cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc
 729
 Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg
 215 220 225

Conseiller ST25

tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp 230 235 240	777
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgc tgc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val 245 250 255	825
aac gag cca ggc cga ttc tcc tgc cac tgc cca caa ggc tac cag ctg ASN Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu 260 265 270 275	873
ctg gct aca agg ctc tgc caa gat att gac gag tgc gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala 280 285 290	921
cac caa tgt tct gag gcc caa acc tgc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr 295 300 305	969
cgc tgc tgc gac acc aac cgt tgc gtc gag ccc tat gtc caa gtc tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser 310 315 320	1017
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgc cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln 325 330 335	1065
cct tca tcc att gtc cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser 340 345 350 355	1113
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly 360 365 370	1161
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe 375 380 385	1209
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg 390 395 400	1257
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr 405 410 415	1305
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr 420 425 430 435	1353
gtc ttt gtg gga gcc tat acc ttc tgaagacct cagggaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe 440	1407
ccccctcccc cctcccatag cttaaagcgc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tcatgtgaag gacaataaag ggagaaagaa ggaaaa	1513

Conseiller.ST25

<211> 443

<212> PRT

<213> Artificial sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16
Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Phe Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Conseiller.ST25
Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220
Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240
Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255
Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270
Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285
Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300
Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
305 310 315 320
Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335
Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
340 345 350
Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365
Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
370 375 380
Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400
Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415
Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430
Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

Conseiller, ST25

<211> 21

<212> DNA

<213> Artificial Sequence

<220> oligonucleotide 3' hMBP1

<400> 17
ctccgctccg aggtgatggc

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220> oligonucleotide 5' hMBP1

<400> 18
tgtagctact ccagctacct c

21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220> Human MBP1 cDNA (partial sequence)
<223>

<400> 19 aagccagccg agccgccaga gcccggggcc gcgggggtgt cgccccccca accccaggat 60
gctccctgc gcctccgtcc tacccgggtc tctactgctc tgggcgtc tactgttgc 120
cttggatca gcttccctc aggattctga agagccgcac agctacacgg aatgcacaga 180
tggatcatgag tgggacccag acaggccgca ctggccggat gtcaacagggt gtctgaccat 240
ccctgaggcc tgcaaggggg aatgaatgtg catcaaccac tacgggggtc acttgtgcct 300
gccccgcgtcc gctggcggtca tcaacgaccc acacggcgag ggaccccccgc caccaggc 360
tcccgcgtcaa caccggcaacc cctgcccacc aggctatgag cccgacgatc aggacagctg 420
tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgccccccgc aggactgcaca 480
taacttccatc agtgcacccgt cccgtatgtt tacccgaaga tcggggcccgaa 540

Conseiller.ST25

gtgtgtggac atagacgagt gccgctaccg	ctactgcctcg caccgctgcg	tgaacctgcc	600		
tggcccttc cgctgcccagt	gcgagccggg	cttccagctg	gggcctaaca	accgctcccg	660
tgttgatgtg aacgagtgtg	acatgggggc	cccatgcgag	cagcgcgtct	tcaactccta	720
tgggaccttc ctgtgtcgct	gccaccaggg	ctatgagctg	catcgggatg	gcttctcctg	780
cagtatatt gatgagtgt	aactccag	ctacctctgt	cagtaccgct	gcgtcaacga	840
gccaggcgt tttccctgcc	actgcccaca	gggttaccag	ctgtggcca	cacgcctctg	900
ccaagacatt gatgagtgt	agtcgtgtc	gcaccaggctc	tccgaggccc	aaacctgtgt	960
caactccat gggggctacc	gctgcgtgga	caccaaccgc	tgcgtggagc	cctacatcca	1020
ggtctcttag aaccgctgtc	tctgccccgc	ctccaaacct	ctatgtcgag	agcagccttc	1080
atccattgtg caccgctaca	tgaccatcac	ctcgaggcgg	ag		1122

<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220> Human MBP1 cDNA (partial sequence)

<400> 20	ccagctacct	ctgtcagtac	cgctgcgtca	acgagccagg	ccgtttctcc	60
tgcctactgcc	cacagggta	ccagctgctg	gccacacgccc	tctgccaaga	cattgatgag	120
tgtgagtctg	gtgcgcacca	gtgcgtccag	gccccaaacct	gtgtcaactt	ccatgggggc	180
taccgcgtc	tggacaccaa	ccgcgtcg	gagccctaca	tccaggcttc	tgagaaccgc	240
tgtctctgcc	cggctccaa	ccctctatgt	cgagagcagc	tttcatccat	tgtgcaccgc	300
tacatgacca	tcacctcgg	gcggagcgtg	cccgctgacg	tgttccagat	ccaggcgtacc	360
tccgtctacc	ccgggtgccta	caatgccttt	cagatccgtg	ctggaaaactc	gcagggggac	420
tttacatta	ggcaaatcaa	caacgtcagc	gccatgtgg	tcctcgccg	gcccgtgacg	480
ggccccccggg	agtacgtct	ggacctggag	atggtcacca	tgaattccct	catgagctac	540
cggggccagct	ctgtactgag	gctcaccgtc	ttttagggg	cctacacctt	ctgaggagca	600
ggaggaggagcc	accctccctg	cagctaccct	agctgaggag	cctgttgta	ggggcagaat	660
gagaaaggca	ataaaaggag	aaag				684

<210> 21

<211> 1480

Conseiller.ST25

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21 aagccagccg	agccgcccaga	gcccggggcc	gcgggggtgt	cgccggccca	accccagg	58											
atg	ctc	ccc	tgc	gcc	tcc	tgc	cta	ccc	ggg	tct	ctt	ctt	ctg	ctc	tgg	gcg	106
Met	Leu	Pro	Cys	Ala	Ser	Cys	Leu	Pro	Gly	Ser	Leu	Leu	Leu	Trp	Ala		
1	5						10							15			
ctg	cta	ctg	ttg	ctc	ttg	gga	tca	gct	tct	cct	cag	gat	tct	gaa	gag		154
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Ala	Ser	Pro	Gln	Asp	Ser	Glu	Glu		
20	25						25							30			
ccc	gac	agc	tac	acg	gaa	tgc	aca	gat	ggc	tat	gag	tgg	gac	cca	gac		202
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Tyr	Trp	Asp	Pro	Asp	
35							40							45			
agc	cag	cac	tgc	cgg	gat	gtc	aac	gag	tgt	ctg	acc	atc	cct	gag	gcc		250
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala		
50							55							60			
tgc	aag	ggg	gaa	atg	aag	tgc	atc	aac	cac	tac	ggg	ggc	tac	ttg	tgc		298
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys		
65							70			75				80			
ctg	ccc	cgc	tcc	gct	gcc	gtc	atc	aac	gac	cta	cac	ggc	gag	gga	ccc		346
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Asn	Asp	Leu	His	Gly	Glu	Gly	Pro		
85							90							95			
ccg	cca	cca	gtg	cct	ccc	gct	caa	cac	ccc	aac	ccc	tgc	cca	cca	gcc		394
Pro	Pro	Pro	Val	Pro	Pro	Ala	Gln	His	Pro	Asn	Pro	Cys	Pro	Pro	Gly		
100							105							110			
tat	gag	ccc	gac	gat	cag	gac	agc	tgt	tgt	gat	gtg	gac	gag	tgt	gcc		442
Tyr	Glu	Pro	Asp	Asp	Gln	Asp	Ser	Cys	Val	Asp	Val	Glu	Cys	Ala			
115							120							125			
cag	gcc	ctg	cac	gac	tgt	cgc	ccc	agc	cag	gac	tgc	cat	aac	ttg	cct		490
Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro		
130							135							140			
ggc	tcc	tat	cag	tgc	acc	tgc	cct	gat	ggt	tac	cgc	aag	atc	ggg	ccc		538
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro		
145							150			155				160			
gag	tgt	gtg	gac	ata	gac	gag	tgc	cgc	tac	cgc	tac	tgc	cag	cac	cgc		586
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg		
165							170							175			
tgc	gtg	aac	ctg	cct	ggc	tcc	ttc	cgc	tgc	cag	tgc	gag	ccg	ggc	tcc		634
Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe		
180							185							190			
cag	ctg	ggg	cct	aac	aac	cgc	tcc	tgt	gtt	gat	gtg	aac	gag	tgt	gac		682

Conseiller.ST25

Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp
195				200					205						
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	tcc	aat	tcc	tat	ggg	acc	ttc
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Tyr	Gly	Thr	Phe	
210				215					220						
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser
225				230					235						240
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr
245				250											255
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	tcc	tgc	cac	tgc	cca	cag	ggt	
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly
260				265					270						
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu
275				280					285						
tct	gtt	ggc	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His
290				295					300						
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile
305				310					315						320
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys
325				330					335						
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser
340				345					350						
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	ggc	acc	tcc	gtc
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val
355				360					365						
tac	ccc	ggt	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gtc	gga	aac	tcg	cag
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln
370				375					380						
ggg	gac	ttt	tac	att	agg	caa	atc	aac	gtc	agc	atg	ctg	gtc		
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val
385				390					395						400
ctc	gcc	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	
405				410					415						
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gtt	ctg
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu
420				425					430						
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gaggagcca			
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe					
435				440											

Conseiller.ST25
ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaaggcaa 1467
taaagggaga aag 1480

<210> 22
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Human MBP1 (complete sequence)

<400> 22
Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Conseiller, ST25

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>
<223> Murine MBP1 cDNA (partial sequence)

<400> 23	gctgtggcag aaaccctcga ctctgccccca ccaccccccgcctcaggat gctccctttt	60
gctccctgc tccccgggtc tttgtgtctc tggcggttc tgctgttgct cttgggagca	120	
gcgtccccac aggatcccgaa ggaggccggac agctacacgg aatgcacaga tggctatgag	180	
tggatgcag acagccagca ctggccggat gtcaacgagt gcctgaccat cccggaggct	240	
tgcaagggtt agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct	300	
gctggcgtca tcaatgtatccat ccatgggttggaa ggaccccccac cgcggccgc ccatgctcaa	360	
caacccaaacc ctggcccgca gggctacgag cctgtatgaac aggagagctg tggatgttg	420	
gacgagtgtt cccaggctt gcatgactgt cggccctgttggactgttggac	480	
ggctccctacc agtgcacccgtt ccctgtatgtt tacggaaaaaa ttggacccggaa atgtgtggac	540	
atagatgagt gtcgttaccg ctattggccatcatgtgtt gtaacctggcc gggctttttt	600	
cgatgcccgtt gtgagccagg ctggccgttggatgttggatgttggatgttg	660	
aatgagtgtt acatggggcgtt gcatgtgttggactgttggac	720	
ctgtgtcgctt gtaaccagggtt atggatgttggactgttggac	780	
gatgagtgtt gcatactccat ttacccgttgc cgttacc	817	

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> sense-GAPDH oligonucleotide

<400> 24
cgaggatgttggcgttggatgttggatgttggatgttg

Conseiller.ST25

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atgggtggta agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cgttgtggcct tgggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

gccctgtatgg ttaccgcaag a

21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

Conseiller.ST25

<400> 28	agccccatg gaagttgaca c	21
<210> 29		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> sense-beta-actin oligonucleotide		
<400> 29	gtggggcgcc ccaggcacca	20
<210> 30		
<211> 1358		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Human MBP1 C-term fragment		
<220>		
<221> CDS		
<222> (1)..(885)		
<400> 30	tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac	48
	Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
1	5 10 15	
ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg	96	
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu		
20 25 30		
cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct	144	
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro		
35 40 45		
aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca	192	
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro		
50 55 60		
tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc	240	
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys		
65 70 75 80		
cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att	288	
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile		
85 90 95		
gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac	336	

Conseiller.ST25												
Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg
100								105				
110												
gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt	tac
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr
115								120				
125												
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser
130							135					
140												
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly
145							150					
155												
160												
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln
165							170					
175												
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg
180							185					
190												
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu
195							200					
205												
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr
210							215					
220												
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Asp
225							230					
235												
240												
att	agg	caa	att	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu
245							250					
255												
gtg	acg	ggc	ccc	ccg	gag	tac	gtg	ctg	gac	ctg	gag	atg
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met
260							265					
270												
aat	tcc	ctc	atg	agc	tac	ccg	gcc	agc	tct	gtt	ctg	agg
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg
275							280					
285												
ttt	gtt	ogg	gcc	tac	acc	ttc	tgaggaggcag	gaggggagcca	ccctccctgc			915
Phe	Val	Gly	Ala	Tyr	Thr	Phe						
290							295					
975												
agcttacccata	gctgaggagc	ctgttgtgag	gggcagaatg	agaaaaggca	taaaggggaga							
aagaaaatcc	ttggggctga	gggtggccggg	tcacactgc	ggaagccctca	ggctggggca							
9035												
gggtggcact	tggggggcga	ggccaaatgc	acctaatacg	gggtctctat	atgttcaggc							
1095												
ccaggggccc	ccatgtacag	gagctggag	cttcgcacca	cgagcttcag	tcaccccgag							
1155												
aggagaggag	gtaacgagga	gggcggactc	caggccccgg	cccagagatt	tggacttggc							
1215												
tggcttgcag	gggtccctaa	aaactccact	ctggacagcg	ccaggaggcc	ctgggttcca							
1275												

Conseiller.ST25
ttcctaactc tgcctcaaac tgtacattt gataaggccc agtagttccc tgggcctgtt 1335
tttctataaa acgaggcaac tgg 1358

<210> 31
<211> 295
<212> PRT
<213> Artificial Sequence
<220>
<223> Human MBP1 C-term fragment

<400> 31

cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
165 170 175

Conseiller.ST25
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>
<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32
gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat 48
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

att gat gtg aac gaa tgc tgg gtc tcg cgc ggc cgc ctg tgc cag cac 192

Conseiller.ST25

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His	
50 55 60	
aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc	240
Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly	
65 70 75 80	
ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtc aac gag tgc	288
Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys	
85 90 95	
gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat	336
Glu Thr Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr	
100 105 110	
cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc	384
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr	
115 120 125	
tgc aca gac atc gat gag tgt gca cag ggc ggc ggc att ctc tgc tat	432
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr	
130 135 140	
ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag	480
Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu	
145 150 155 160	
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat	528
Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp	
165 170 175	
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac	576
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His	
180 185 190	
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac	624
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn	
195 200 205	
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat	672
Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp	
210 215 220	
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc	720
Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu	
225 230 235 240	
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc	768
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly	
245 250 255	
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag	816
Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys	
260 265 270	
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act	864
Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr	
275 280 285	
ggt gtc gta tcc ctg cag cgg tct gtt ctg gag ccc cgg gac ttt gcc	912
Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala	
290 295 300	

Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc	960
Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe	
305 310 315 320	
ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtaca	1009
Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro	
325 330	
tgtcaggcaa tccctccagg tgatgcctgg gcgggtggca gctgcgccac tcctaagtgg	1069
ctttttgctg tgactctgtta acttaactta atcatgtga gctgggttggt cttagtctc	1129
tacccttagag ggagggagat gcaccccgag aggcaactgag tacaggccag ggtcaccggaa	1189
ggcttagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc	1249
aactatggct acagctgaca ttccattcct tcattccactg tgtttctcaa taaaaaaaaaa	1309
aaatcagctg tgcatggtag cacagacctt taatccttagc actggggagg cagaggttagg	1369
tagatctctg agttccaggc cagccgtgc tacactggga gttctaaccacccagagacta	1429
catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc	1489
agcctggct acgctgggg ttcttaaccag ccagagactac atagagagat cctatctcaa	1549
caaggaaaaaa taaaagaaaat cattttaaaaa ggttttttttttt tttgtgttg ttgttaatgg	1609
ataagagtag cacatataca ttataaaaa tgatcaaata gcacagaaag gtta	1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>
<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
65 70 75 80

Conseiller.ST25

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Phe Ala Pro
Page 26

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Pro Ser Leu Arg
1 5 10 15

<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro
1 5 10 15

Asn Pro Arg